

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

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(i) APPLICANT:

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(i) APPLICANT:

(A) NAME: Adelman, John P.
(B) STREET: 2433 S.W. Mitchell Street
(C) CITY: Portland
(D) STATE: Oregon
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(F) POSTAL CODE (ZIP): 97201
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(I) TELEX:

(i) APPLICANT:

(A) NAME: Maylie, James
(B) STREET: 1445 S.W. Westwood Drive
(C) CITY: Portland
(D) STATE: Oregon
(E) COUNTRY: USA
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(I) TELEX:

(i) APPLICANT:

(A) NAME: Bond, Chris T.
(B) STREET: 2433 S.W. Mitchell Street
(C) CITY: Portland
(D) STATE: Oregon
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 97201
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(I) TELEX:

- (i) APPLICANT:
(A) NAME: Silvia, Christopher P.
(B) STREET: 3105 Broomsedge Way
(C) CITY: Durham
(D) STATE: North Carolina
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 27712
(G) TELEPHONE:
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(I) TELEX:
- (ii) TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/US97/Not yet assigned
(B) FILING DATE: Not yet assigned
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/026,451
(B) FILING DATE: 11-SEP-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/040,052
(B) FILING DATE: 07-MAR-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/045,233
(B) FILING DATE: 17-APR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Weber, Kenneth A.
(B) REGISTRATION NUMBER: 31,677
(C) REFERENCE/DOCKET NUMBER: 014210-000730PC
- (ix) TELECOMMUNICATION INFORMATION:
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- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 561 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein
 (B) LOCATION: 1..561
 (D) OTHER INFORMATION: /note= "human small conductance,
 calcium-activated potassium channel protein 1 (hSK1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Pro Gly Pro Arg Ala Ala Cys Ser Glu Pro Asn Pro Cys Thr Gln
1           5           10           15
Val Val Met Asn Ser His Ser Tyr Asn Gly Ser Val Gly Arg Pro Leu
20           25           30
Gly Ser Gly Pro Gly Ala Leu Gly Arg Asp Pro Pro Asp Pro Glu Ala
35           40           45
Gly His Pro Pro Gln Pro Pro His Ser Pro Gly Leu Gln Val Val Val
50           55           60
Ala Lys Ser Glu Pro Ala Arg Pro Ser Pro Gly Ser Pro Arg Gly Gln
65           70           75           80
Pro Gln Asp Gln Asp Asp Asp Glu Asp Asp Glu Glu Asp Glu Ala Gly
85           90           95
Arg Gln Arg Ala Ser Gly Lys Pro Ser Asn Val Gly His Arg Leu Gly
100          105          110
His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala
115          120          125
Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Thr Glu Thr Glu
130          135          140
Leu Ser Trp Gly Val Tyr Thr Lys Glu Ser Leu Tyr Ser Phe Ala Leu
145          150          155          160
Lys Cys Leu Ile Ser Leu Ser Thr Ala Ile Leu Leu Gly Leu Val Val
165          170          175
Leu Tyr His Ala Arg Glu Ile Gln Leu Phe Met Val Asp Asn Gly Ala
180          185          190
Asp Asp Trp Arg Ile Ala Met Thr Cys Glu Arg Val Phe Leu Ile Ser
195          200          205
Leu Glu Leu Ala Val Cys Ala Ile His Pro Val Pro Gly His Tyr Arg
210          215          220
Phe Thr Trp Thr Ala Arg Leu Ala Phe Thr Tyr Ala Pro Ser Val Ala
225          230          235          240
Glu Ala Asp Val Asp Val Leu Leu Ser Ile Pro Met Phe Leu Arg Leu
245          250          255
Tyr Leu Leu Gly Arg Val Met Leu Leu His Ser Lys Ile Phe Thr Asp
260          265          270
Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Thr Phe Asn Thr
275          280          285
Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu
290          295          300

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93

Leu Val Phe Ser Ile Ser Ser Trp Ile Ile Ala Ala Trp Thr Val Arg
 305 310 315 320
 Val Cys Glu Arg Tyr His Asp Lys Gln Glu Val Thr Ser Asn Phe Leu
 325 330 335
 Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly
 340 345 350
 Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr
 355 360 365
 Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala
 370 375 380
 Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met
 385 390 395 400
 Met Asp Thr Gln Leu Thr Lys Arg Val Lys Asn Ala Ala Ala Asn Val
 405 410 415
 Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Arg Leu Val Lys Lys
 420 425 430
 Pro Asp Gln Ala Arg Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala
 435 440 445
 Ile His Gln Ala Gln Lys Leu Arg Ser Val Lys Ile Glu Gln Gly Lys
 450 455 460
 Leu Asn Asp Gln Ala Asn Thr Leu Thr Asp Leu Ala Lys Thr Gln Thr
 465 470 475 480
 Val Met Tyr Asp Leu Val Ser Glu Leu His Ala Gln His Glu Glu Leu
 485 490 495
 Glu Ala Arg Leu Ala Thr Leu Glu Ser Arg Leu Asp Ala Leu Gly Ala
 500 505 510
 Ser Leu Gln Ala Leu Pro Gly Leu Ile Ala Gln Ala Ile Arg Pro Pro
 515 520 525
 Pro Pro Pro Leu Pro Pro Arg Pro Gly Pro Gly Pro Gln Asp Gln Ala
 530 535 540
 Ala Arg Ser Ser Pro Cys Arg Trp Thr Pro Val Ala Pro Ser Asp Cys
 545 550 555 560
 Gly

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..580
- (D) OTHER INFORMATION: /note= "rat small conductance, calcium-activated potassium channel protein 2 (rSK2)"

(ix) FEATURE:

- (A) NAME/KEY: Region
 (B) LOCATION: 135..462
 (D) OTHER INFORMATION: /note= "core region of rSK2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ser Cys Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn
 1 5 10 15
 Leu Ser Ser Ser Arg Arg Asn Leu His Glu Met Asp Ser Glu Ala Gln
 20 25 30
 Pro Leu Gln Pro Pro Ala Ser Val Val Gly Gly Gly Gly Ala Ser
 35 40 45
 Ser Pro Ser Ala Ala Ala Ala Ala Ser Ser Ser Ala Pro Glu Ile Val
 50 55 60
 Val Ser Lys Pro Glu His Asn Asn Ser Asn Asn Leu Ala Leu Tyr Gly
 65 70 75 80
 Thr Gly Gly Gly Gly Ser Thr Gly Gly Gly Gly Gly Gly Gly Gly
 85 90 95
 Gly Gly Gly Ser Gly His Gly Ser Ser Ser Gly Thr Lys Ser Ser Lys
 100 105 110
 Lys Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly His Arg Arg Ala Leu
 115 120 125
 Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala Leu Ile Phe Gly Met
 130 135 140
 Phe Gly Ile Val Val Met Val Ile Glu Thr Glu Leu Ser Trp Gly Ala
 145 150 155 160
 Tyr Asp Lys Ala Ser Leu Tyr Ser Leu Ala Leu Lys Cys Leu Ile Ser
 165 170 175
 Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile Val Tyr His Ala Arg
 180 185 190
 Glu Ile Gln Leu Phe Met Val Asp Asn Gly Ala Asp Asp Trp Arg Ile
 195 200 205
 Ala Met Thr Tyr Glu Arg Ile Phe Phe Ile Cys Leu Glu Ile Leu Val
 210 215 220
 Cys Ala Ile His Pro Ile Pro Gly Asn Tyr Thr Phe Thr Trp Thr Ala
 225 230 235 240
 Arg Leu Ala Phe Ser Tyr Ala Pro Ser Thr Thr Thr Ala Asp Val Asp
 245 250 255
 Ile Ile Leu Ser Ile Pro Met Phe Leu Arg Leu Tyr Leu Ile Ala Arg
 260 265 270
 Val Met Leu Leu His Ser Lys Leu Phe Thr Asp Ala Ser Ser Arg Ser
 275 280 285
 Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr Arg Phe Val Met Lys
 290 295 300
 Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe Ser Ile
 305 310 315 320

95

Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Ala Cys Glu Arg Tyr
 325 330 335
 His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly Ala Met Trp Leu
 340 345 350
 Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro Asn
 355 360 365
 Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly Ala
 370 375 380
 Gly Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu Leu
 385 390 395 400
 Thr Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Thr Gln Leu
 405 410 415
 Thr Lys Arg Val Lys Asn Ala Ala Ala Asn Val Leu Arg Glu Thr Trp
 420 425 430
 Leu Ile Tyr Lys Asn Thr Lys Leu Val Lys Lys Ile Asp His Ala Lys
 435 440 445
 Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile His Gln Leu Arg
 450 455 460
 Ser Val Lys Met Glu Gln Arg Lys Leu Asn Asp Gln Ala Asn Thr Leu
 465 470 475 480
 Val Asp Leu Ala Lys Thr Gln Asn Ile Met Tyr Asp Met Ile Ser Asp
 485 490 495
 Leu Asn Glu Arg Ser Glu Asp Phe Glu Lys Arg Ile Val Thr Leu Glu
 500 505 510
 Thr Lys Leu Glu Thr Leu Ile Gly Ser Ile His Ala Leu Pro Gly Leu
 515 520 525
 Ile Ser Gln Thr Ile Arg Gln Gln Gln Arg Asp Phe Ile Glu Thr Gln
 530 535 540
 Met Glu Asn Tyr Asp Lys His Val Thr Tyr Asn Ala Glu Arg Ser Arg
 545 550 555 560
 Ser Ser Ser Arg Arg Arg Arg Ser Ser Ser Thr Ala Pro Pro Thr Ser
 565 570 575
 Ser Glu Ser Ser
 580

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 553 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..553
 (D) OTHER INFORMATION: /note= "N-terminally truncated form of rat small conductance, calcium-activated potassium channel protein 3 (rSK3)"

(ix) FEATURE:
 (A) NAME/KEY: Region
 (B) LOCATION: 109..436
 (D) OTHER INFORMATION: /note= "core region of rSK3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Ser Ser Cys Lys Tyr Ser Gly Gly Val Met Lys Pro Leu Ser Arg
1          5          10          15
Leu Ser Ala Ser Arg Arg Asn Leu Ile Glu Ala Glu Pro Glu Gly Gln
20          25          30
Pro Leu Gln Leu Phe Ser Pro Ser Asn Pro Pro Glu Ile Ile Ile Ser
35          40          45
Ser Arg Glu Asp Asn His Ala His Gln Thr Leu Leu His His Pro Asn
50          55          60
Ala Thr His Asn His Gln His Ala Gly Thr Thr Ala Gly Ser Thr Thr
65          70          75          80
Phe Pro Lys Ala Asn Lys Arg Lys Asn Gln Asn Ile Gly Tyr Lys Leu
85          90          95
Gly His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr
100         105         110
Ala Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Ile Glu Thr
115         120         125
Glu Leu Ser Trp Gly Leu Tyr Ser Lys Asp Ser Met Phe Ser Leu Ala
130         135         140
Leu Lys Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile
145         150         155         160
Ile Ala Tyr His Thr Arg Glu Val Gln Leu Phe Val Ile Asp Asn Gly
165         170         175
Ala Asp Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile Leu Tyr Ile
180         185         190
Ser Leu Glu Met Leu Val Cys Ala Ile His Pro Ile Pro Gly Glu Tyr
195         200         205
Lys Phe Phe Trp Thr Ala Arg Leu Ala Phe Ser Tyr Thr Pro Ser Arg
210         215         220
Ala Glu Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg
225         230         235         240
Leu Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr
245         250         255
Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn
260         265         270

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Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val
 275 280 285
 Leu Leu Met Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val
 290 295 300
 Arg Val Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe
 305 310 315 320
 Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr
 325 330 335
 Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu
 340 345 350
 Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val
 355 360 365
 Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe
 370 375 380
 Met Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala Ala Ala Asn
 385 390 395 400
 Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys
 405 410 415
 Lys Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys Phe Leu Gln
 420 425 430
 Ala Ile His Gln Leu Arg Gly Val Lys Met Glu Gln Arg Lys Leu Ser
 435 440 445
 Asp Gln Ala Asn Thr Leu Val Asp Leu Ser Lys Met Gln Asn Val Met
 450 455 460
 Tyr Asp Leu Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp Leu Glu Lys
 465 470 475 480
 Gln Ile Gly Ser Leu Glu Ser Lys Leu Glu His Leu Thr Ala Ser Phe
 485 490 495
 Asn Ser Leu Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln Gln Gln Gln
 500 505 510
 Gln Leu Leu Thr Ala Phe Val Glu Ala Arg Gly Ile Ser Val Ala Val
 515 520 525
 Gly Thr Ser His Ala Pro Pro Ser Asp Ser Pro Ile Gly Ile Ser Ser
 530 535 540
 Thr Ser Phe Pro Glu Phe Leu Ile Phe
 545 550

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 458 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein
 (B) LOCATION: 1..458
 (D) OTHER INFORMATION: /note= "rat small conductance,
 calcium-activated potassium channel protein 1 (rSK1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Gly Lys Pro Pro Thr Val Ser His Arg Leu Gly His Arg Arg Ala
 1 5 10 15
 Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala Leu Ile Phe Gly
 20 25 30
 Met Phe Gly Ile Val Val Met Val Thr Glu Thr Glu Leu Ser Trp Gly
 35 40 45
 Val Tyr Thr Lys Glu Ser Leu Cys Ser Phe Ala Leu Lys Cys Leu Ile
 50 55 60
 Ser Leu Ser Thr Val Ile Leu Leu Gly Leu Val Ile Leu Tyr His Ala
 65 70 75 80
 Arg Glu Ile Gln Leu Phe Leu Val Asp Asn Gly Ala Asp Asp Trp Arg
 85 90 95
 Ile Ala Met Thr Trp Glu Arg Val Ser Leu Ile Ser Leu Glu Leu Ala
 100 105 110
 Val Cys Ala Ile His Pro Val Pro Gly His Tyr Arg Phe Thr Trp Thr
 115 120 125
 Ala Arg Leu Ala Phe Ser Leu Val Pro Ser Ala Ala Glu Ala Asp Val
 130 135 140
 Asp Val Leu Leu Ser Ile Pro Met Phe Leu Arg Leu Tyr Leu Leu Ala
 145 150 155 160
 Arg Val Met Leu Leu His Ser Arg Ile Phe Thr Asp Ala Ser Ser Arg
 165 170 175
 Ser Ile Gly Ala Leu Asn Arg Val Thr Phe Asn Thr Arg Phe Val Thr
 180 185 190
 Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe Ser
 195 200 205
 Ile Ser Ser Trp Ile Val Ala Ala Trp Thr Val Arg Val Cys Glu Arg
 210 215 220
 Tyr His Asp Lys Gln Glu Val Thr Ser Asn Phe Leu Gly Ala Met Trp
 225 230 235 240
 Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro
 245 250 255
 His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly
 260 265 270
 Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu
 275 280 285
 Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Thr Gln
 290 295 300

99

Leu Thr Lys Arg Val Lys Asn Ala Ala Ala Asn Val Leu Arg Glu Thr
 305 310 315 320
 Trp Leu Ile Tyr Lys His Thr Arg Leu Val Lys Lys Pro Asp Gln Ser
 325 330 335
 Arg Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile His Gln Ala
 340 345 350
 Gln Lys Leu Arg Thr Val Lys Ile Glu Gln Gly Lys Val Asn Asp Gln
 355 360 365
 Ala Asn Thr Leu Ala Asp Leu Ala Lys Ala Gln Ser Ile Ala Tyr Glu
 370 375 380
 Val Val Ser Glu Leu Gln Ala Gln Gln Glu Glu Leu Glu Ala Arg Leu
 385 390 395 400
 Ala Ala Leu Glu Ser Arg Leu Asp Val Leu Gly Ala Ser Leu Gln Ala
 405 410 415
 Leu Pro Ser Leu Ile Ala Gln Ala Ile Cys Pro Leu Pro Pro Pro Trp
 420 425 430
 Pro Gly Pro Ser His Leu Thr Thr Ala Ala Gln Ser Pro Gln Ser His
 435 440 445
 Trp Leu Pro Thr Thr Ala Ser Asp Cys Gly
 450 455

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGCCGGGTC CCCGGGCGGC CTGC

24

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCACCCGCAG TCCGAGGGGG CCAC

24

100

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAGCAGCT GCAGGTACAA CGGG

24

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAGCTACTC TCAGATGAAG TTGG

24

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAGCTCCT GCAAATACAG CGGT

24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTAGCAACTG CTTGAACTTG

20

101

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCAGGGAAGC CCCCACCGT CAGT

24

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCACCCACAG TCTGATGCCG TGGT

24

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1683 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1683
(D) OTHER INFORMATION: /note= "human small conductance,
calcium-activated potassium channel protein 1 (hSK1) cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGCCGGGTC CCCGGGCGGC CTGCAGCGAG CCCAACCCCT GCACCCAGGT AGTCATGAAC 60
AGCCACAGCT ACAATGGCAG CGTGGGGCGG CCGCTGGGCA GCGGGCCGGG CGCCCTGGGA 120
CGAGACCCTC CGGACCCTGA GGCCGGCCAC CCCCCACAAC CCCCACAG CCCGGGCCTC 180
CAGGTGGTAG TGGCCAAGAG TGAGCCAGCC CGGCCCTCAC CCGGCAGCCC CCGGGGGCAG 240
CCCCAGGACC AGGACGATGA CGAGGATGAT GAGGAAGATG AGGCCGGCAG GCAGAGAGCC 300
TCGGGGAAAC CCTCAAATGT GGGCCACCGC CTGGGGCCACC GGCGGGCGCT CTTGAGAAG 360
CGGAAGCGCC TCAGCGACTA TGCCCTCATT TTCGGCATGT TTGGCATCGT CGTCATGGTG 420
ACGGAGACCG AGCTGTCCTG GGGGTGTAC ACCAAGGAGT CTCTGTACTC ATTCGCACTC 480

102

AAATGCCTCA TGAGCCTCTC CACGGCCATC CTGCTGGGTC TCGTTGTCTT CTACCATGCC 540
CGGGAGATCC AGCTGTTTCAT GGTGGACAAC GGGGCTGATG ACTGGCGCAT CGCCATGACC 600
TGCGAGCGCG TGTTCCTCAT CTCGCTAGAG CTGGCAGTGT GCGCCATTCA CCCGGTGCCC 660
GGCCACTACC GCTTCACGTG GACGGCGCGG CTGGCCTTCA CGTACGCGCC CTCGGTGGCC 720
GAGGCCGACG TGGACGTGCT GCTGTCCATC CCCATGTTCC TGCGCCTCTA CCTGCTGGGC 780
CGGGTGATGC TACTGCACAG CAAAATCTTC ACGGACGCCT CGAGCCGCAG CATCGGGGCC 840
CTCAACAAGA TCACCTTCAA CACGCGCTTC GTCATGAAGA CACTCATGAC CATCTGCCCC 900
GGCACCGTGC TGCTGGTCTT CAGCATCTCC TCCTGGATCA TCGCAGCCTG GACCGTGCGC 960
GTCTGCGAGA GGTACCACGA CAAGCAGGAA GTGACCAGCA ACTTCCTGGG GGCCATGTGG 1020
CTGATTTCCA TCACCTTCCT CTCCATTGGC TACGGCGACA TGGTGCCCCA CACCTACTGC 1080
GGGAAGGGTG TGTGCCTGCT CACTGGCATC ATGGGAGCTG GCTGTACCGC GCTCGTGGTG 1140
GCTGTGGTGG CTCGGAAGCT GGAGCTCACC AAGGCTGAGA AGCACGTGCA CAACTTCATG 1200
ATGGACACTC AGCTCACCAA GCGGGTAAAA AACGCCGCTG CTAACGTTCT CAGGGAGACG 1260
TGGCTCATCT ACAAACATAC CAGGCTGGTG AAGAAGCCAG ACCAAGCCCG GGTTCGGAAA 1320
CACCAGCGTA AGTTCCTCCA AGCCATCCAT CAGGCTCAGA AGCTCCGGAG TGTGAAGATC 1380
GAGCAAGGGA AGCTGAACGA CCAGGCTAAC ACGCTTACCG ACCTAGCCAA GACCCAGACC 1440
GTCATGTACG ACCTTGATC GGAGCTGCAC GCTCAGCACG AGGAGCTGGA GGCCCGCCTG 1500
GCCACCCTGG AAAGCCGCTT GGATGCGCTG GGTGCCTCTC TACAGGCCCT GCCTGGCCTC 1560
ATCGCCCAAG CCATACGCCC ACCCCCGCCT CCCCTGCCTC CCAGGCCCGG CCCC GGCCCC 1620
CAAGACCAGG CAGCCCGGAG CTCCCCCTGC CGGTGGACGC CCGTGGCCCC CTCGGACTGC 1680
GGG 1683

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1374
- (D) OTHER INFORMATION: /note= "rat small conductance, calcium-activated potassium channel protein 1 (rSK1) cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCAGGGAAGC CCCC GACCGT CAGTCACCGC CTGGGCCACC GTAGGGCCCT CTTGAGAAG 60
CGTAAACGAC TCAGTGAATA TGCACTCATC TTTGGCATGT TCGGGATTGT CGTCATGGTG 120

103

ACAGAAACAG AGCTGTCCTG GGGTGTGTAC ACCAAGGAGT CTCTGTGCTC ATTCGCCCTG 180
AAATGCCTAA TCAGCCTCTC CACTGTCATC CTGCTTGGCC TTGTCATCCT CTACCACGCC 240
CGAGAGATCC AGCTGTTCTT GGTGGACAAT GGTGCCGATG ACTGGCGCAT TGCCATGACC 300
TGGGAGCGAG TGTCCCTGAT CTCGCTGGAG TTGGCTGTGT GTGCCATCCA CCCAGTGCCT 360
GGCCACTACC GCTTCACATG GACGGCGCGG CTGGCCTTCT CCCTGGTGCC GTCAGCAGCC 420
GAGGCGGATG TGGATGTGCT TCTGTCCATC CCCATGTTTC TGCCTCTTA TCTGCTGGCT 480
CGGGTCATGC TCCTGCACAG CCGCATCTTC ACGGACGCAT CCAGTCGCAG CATCGGAGCC 540
CTGAACCGTG TCACCTTCAA CACACGCTTT GTCACCAAGA CACTCATGAC CATCTGCCCT 600
GGCACCCTGC TGTGGTCTT CAGCATCTCC TCCTGGATCG TCGCTGCATG GACAGTGC GC 660
GTGTGTGAGA GGTACCATGA TAAACAGGAA GTGACCAGCA ACTTCCTGGG GGCCATGTGG 720
CTCATCTCCA TTACCTTCCT GTCCATCGGC TACGGGGACA TGGTGCCGCA CACCTACTGT 780
GGGAAGGGCG TGTGTCTGCT CACCGGCATC ATGGGAGCAG GCTGCACTGC ACTCGTGGTG 840
GCCGTCGTGG CCCGCAAGTT GGAAGTCACC AAGGCTGAGA AACACGTGCA CAACCTCATG 900
ATGGACACAC AGCTCACCAA GCGGGTTAAA AACGCCGCTG CAAACGTTCT CAGGGAGACA 960
TGGCTCATCT ACAAACACAC CAGGCTAGTG AAGAAGCCAG ACCAAAGCCG GGTTCGGAAA 1020
CACCAGCGTA AGTTCCTTCA GGCCATCCAT CAGGCGCAGA AGCTCCGGAC TGTGAAGATT 1080
GAACAAGGGA AGGTGAATGA TCAGGCCAAC ACGCTGGCTG ACCTGGCCAA GGCACAGAGC 1140
ATCGCATATG AGGTGGTGTG GGAGCTGCAG GCCCAGCAGG AGGAGTTGGA GGCCCGTCTG 1200
GCTGCCCTGG AGAGCCGCCT GGATGTCCTA GGCGCCTCCC TGCAGGCCCT ACCAAGTCTC 1260
ATAGCCCAAG CCATATGCCC TCTACCACCA CCCTGGCCCC GGCCCAGTCA CCTGACCACA 1320
GCCGCCCAGA GCCCACAAAG CCACTGGCTG CCCACCACGG CATCAGACTG TGGG 1374

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1740 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1740
(D) OTHER INFORMATION: /note= "rat small conductance,
calcium-activated potassium channel protein 2 (rSK2) cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGAGCAGCT GCAGGTACAA CGGGGGCGTC ATGCGTCCGC TCAGCAACTT GAGCTCGTCC 60
CGCCGGAACC TGCACGAGAT GGAATCAGAG GCTCAGCCCC TGCAGCCCCC AGCGTCGGTT 120

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GTAGGAGGAG GTGGTGGTGC GTCCTCCCCG TCTGCTGCCG CCGCCGCCTC ATCCTCAGCC 180
CCAGAGATCG TGGTGTCTAA GCCGGAGCAC AACAAATTCTA ACAACCTGGC GCTCTACGGA 240
ACTGGCGGCG GAGGCAGCAC CGGAGGCGGC GCGGGCGGCG GCGGCGGCGG CGGCGGCAGC 300
GGGCATGGCA GCAGCAGCGG CACTAAGTCC AGCAAAAAGA AGAACCAGAA CATCGGCTAT 360
AAGCTGGGCC ATCGGCGTGC CCTGTTTGAG AAGCGCAAGC GGCTCAGCGA CTATGCGCTC 420
ATCTTCGGCA TGTTCGGCAT CGTGGTCATG GTCATCGAGA CCGAGCTGTC GTGGGGCGCC 480
TACGACAAGG CGTCGCTGTA TTCTTTAGCT CTGAAATGCC TTATCAGTCT CTCCACGATC 540
ATCCTGCTTG GTCTGATCAT CGTATACCAC GCCAGGGAAA TACAGTTATT CATGGTGGAC 600
AATGGAGCAG ATGACTGGAG AATAGCCATG ACTTATGAAC GTATTTTCTT CATCTGCTTG 660
GAAATACTGG TGTGTGCTAT TCATCCCATC CCTGGGAATT ATACGTTTAC ATGGACAGCC 720
CGGCTTGCCCT TCTCCTATGC CCCTTCCACA ACCACTGCAG ACGTGGATAT TATTTTATCT 780
ATACCAATGT TCTTAAGACT CTATCTGATT GCCAGAGTCA TGCTATTACA TAGCAAATT 840
TTCACCGATG CCTCCTCTAG AAGCATTGGG GCACTTAATA AGATAAACTT CAATACGCGT 900
TTTGTATGA AGACTTTAAT GACTATCTGC CCAGGAACTG TGCTCTTGGT TTTTAGTATC 960
TCGTTATGGA TAATTGCCGC ATGGACTGTC CGAGCTTGTC AAAGGTACCA TGATCAACAG 1020
GATGTCACCTA GCAACTTCCT TGGAGCAATG TGGTTGATAT CAATAACTTT TCTCTCCATT 1080
GGTTATGGTG ACATGGTACC TAACACATAC TGTGGGAAAG GAGTCTGCTT GCTTACCGGA 1140
ATAATGGGTG CAGGTTGCAC AGCCTTGGTG GTAGCCGTAG TGGCAAGGAA GCTAGAACTT 1200
ACCAAAGCAG AAAAGCATGT GCACAATTTT ATGATGGATA CTCAGCTGAC CAAAAGAGTA 1260
AAAAACGCAG CCGCCAATGT ACTCAGGGAA ACGTGGTTAA TCTACAAAAA CACAAAGCTA 1320
GTGAAAAAGA TCGACCATGC AAAAGTAAGG AAGCATCAAC GGAAATTCTT ACAAGCTATT 1380
CATCAATTAA GAAGTGTGAA GATGGAACAG AGGAAACTGA ATGACCAAGC GAATACGCTA 1440
GTGGATCTGG CAAAGACCCA AGATATCATG TATGATATGA TTTCCGACTT AAATGTAAGG 1500
AGTGAAGACT TTGAGAAAAG GATCGTCACC CTGGAAACAA AATTAGAAAC TTTGATTGGT 1560
AGCATTCTATG CCCTCCCTGG GCTTATCAGC CAGACCATCA GACAGCAGCA AAGGGACTTC 1620
ATAGAGACAC AGATGGAGAA CTATGACAAG CATGTCACCT ACAATGCTGA GCGTTCCCGG 1680
TCCTCGTCCA GGAGGCGGCG GTCCTCCTCC ACAGCGCCAC CAACTTCATC TGAGAGTAGC 1740

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1659 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1659
(D) OTHER INFORMATION: /note= "N-terminally truncated cDNA
for rat small conductance, calcium-activated potassium channel
protein 3 (rSK3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGAGCTCCT GCAAATACAG CGGTGGGGTC ATGAAGCCCC TCAGCCGCCT CAGCGCCTCT	60
CGGAGAAACC TTATCGAGGC CGAGCCTGAG GGCCAACCCC TCCAGCTCTT CAGTCCCAGC	120
AACCCCCCAG AGATTATCAT CTCCTCCAGG GAGGATAACC ATGCCCACCA GACTCTGCTC	180
CATCACCCCA ACGCTACCCA CAACCACCAG CATGCCGGCA CCACTGCTGG CAGCACCACC	240
TTCCCCAAAG CCAACAAGCG GAAAAACCAA AACATTGGCT ATAAGCTGGG GCACAGGAGG	300
GCCCTGTTTG AAAAGAGAAA GCGACTGAGT GACTATGCTC TGATTTTGGG GATGTTTGGA	360
ATTGTTGTTA TGGTGATAGA GACCGAACTG TCTTGGGGTT TGTACTCAA GGATTCCATG	420
TTTTCGTTGG CCCTGAAATG CTTTATCAGT TTATCCACCA TCATCCTGCT TGGTTTGATC	480
ATCGCCTACC ACACAAGGGA AGTACAGCTC TTTGTGATCG ACAATGGTGC AGATGACTGG	540
CGGATAGCCA TGACCTATGA GCGCATCCTC TACATCAGCC TGGAGATGCT GGTGTGCGCC	600
ATCCACCCCA TTCCTGGAGA GTACAAGTTC TTCTGGACGG CACGCCTGGC CTTCTCCTAC	660
ACCCCTCTC GGGCAGAGGC TGACGTGGAC ATTATTCTGT CCATCCCCAT GTTCTTGCGC	720
CTATACCTGA TCGCCCGAGT CATGCTGCTA CATAGCAAGC TCTTCACGGA TGCCTCATCC	780
CGAAGCATCG GGGCCCTCAA CAAGATCAAC TTCAACACCC GATTCGTCAT GAAGACGCTC	840
ATGACCATCT GCGCGGGCAC GGTGCTGCTA ATGTTTCAGCA TCTCTCTGTG GATCATCGCT	900
GCCTGGACTG TGAGAGTCTG TGAAAGGTAC CATGACCAGC AGGACGTAAC TAGTAACTTT	960
CTGGGTGCCA TGTGGCTCAT CTCCATCAGC TTCCTTTCCA TTGGCTATGG GGACATGGTG	1020
CCCCACACAT ACTGTGGGAA AGGTGTCTGT CTTCTCACTG GCATCATGGG TGCAGGCTGC	1080
ACTGCCCTCG TGGTAGCTGT GGTGCCCCG AAGCTCGAAC TCACCAAAGC AGAGAAGCAT	1140
GTGCACAACT TCATGATGGA CACTCAGCTC ACCAAACGGA TCAAGAACGC TGCCGCCAAT	1200
GTCCTCCGGG AAACATGGCT GATCTACAAA CACACAAAGC TGCTAAAGAA GATTGACCAC	1260
GCCAAAGTCA GGAAACACCA GAGGAAGTTC CTCCAAGCTA TTCACCAACT GAGGGGTGTC	1320
AAGATGGAAC AAAGGAAGCT GAGTGACCAA GCCAACACCC TGGTGGACCT TTCCAAGATG	1380
CAGAACGTCA TGTATGACTT GATCACGGAG CTCAACGACC GGAGTGAAGA CCTGGAAAAG	1440
CAGATTGGCA GCCTGGAATC CAAGCTGGAG CACCTCACAG CCAGCTTCAA TTCCCTGCCC	1500
CTGCTCATCG CAGACACCCT GCGCCAACAG CAGCAGCAGC TGCTCACTGC CTTCGTGGAG	1560
GCCCCGGGCA TCAGTGTGGC TGTGGGAACT AGCCACGCCC CTCCCTCTGA CAGCCCTATC	1620
GGGATCAGCT CCACCTCTTT CCCGGAATTC CTAATATTC	1659

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Ser Asp Tyr Ala Leu Ile Phe Gly Met
 1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gln Arg Lys Phe Leu Gln Ala Ile His Gln
 1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..579
- (D) OTHER INFORMATION: /note= "human small conductance, calcium-activated potassium channel protein 2 (hSK2)"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 134..461
- (D) OTHER INFORMATION: /note= "core region of hSK2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ser Ser Cys Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn
 1 5 10 15

Leu Ser Ala Ser Arg Arg Asn Leu His Glu Met Asp Ser Glu Ala Gln
 20 25 30

Pro Leu Gln Pro Pro Ala Ser Val Gly Gly Gly Gly Ala Ser Ser
 35 40 45

Pro Ser Ala Ala Ala Ala Ala Ala Val Ser Ser Ser Ala Pro
50 55 60

Glu Ile Val Val Ser Lys Pro Glu His Asn Asn Ser Asn Asn Leu Ala
65 70 75 80

Leu Tyr Gly Thr Gly Gly Gly Gly Ser Thr Gly Gly Gly Gly Gly Gly
85 90 95

Gly Gly Ser Gly His Gly Ser Ser Ser Gly Thr Lys Ser Ser Lys Lys
100 105 110

Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly His Arg Arg Ala Leu Phe
115 120 125

Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala Leu Ile Phe Gly Met Phe
130 135 140

Gly Ile Val Val Met Val Ile Glu Thr Glu Leu Ser Trp Gly Ala Tyr
145 150 155 160

Asp Lys Ala Ser Leu Tyr Ser Leu Ala Leu Lys Cys Leu Ile Ser Leu
165 170 175

Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile Val Tyr His Ala Arg Glu
180 185 190

Ile Gln Leu Phe Met Val Asp Asn Gly Ala Asp Asp Trp Arg Ile Ala
195 200 205

Met Thr Tyr Glu Arg Ile Phe Phe Ile Cys Leu Glu Ile Leu Val Cys
210 215 220

Ala Ile His Pro Ile Pro Gly Asn Tyr Thr Phe Thr Trp Thr Ala Arg
225 230 235 240

Leu Ala Phe Ser Tyr Ala Pro Ser Thr Thr Thr Ala Asp Val Asp Ile
245 250 255

Ile Leu Ser Ile Pro Met Phe Leu Arg Leu Tyr Leu Ile Ala Arg Val
260 265 270

Met Leu Leu His Ser Lys Leu Phe Thr Asp Ala Ser Ser Arg Ser Ile
275 280 285

Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr Arg Phe Val Met Lys Thr
290 295 300

Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe Ser Ile Ser
305 310 315 320

Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Ala Cys Glu Arg Tyr His
325 330 335

Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly Ala Met Trp Leu Ile
340 345 350

Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro Asn Thr
355 360 365

Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly Ala Gly
370 375 380

Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu Leu Thr
385 390 395 400

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Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Thr Gln Leu Thr
 405 410 415
 Lys Arg Val Lys Asn Ala Ala Ala Asn Val Leu Arg Glu Thr Trp Leu
 420 425 430
 Ile Tyr Lys Asn Thr Lys Leu Val Lys Lys Ile Asp His Ala Lys Val
 435 440 445
 Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile His Gln Leu Arg Ser
 450 455 460
 Val Lys Met Glu Gln Arg Lys Leu Asn Asp Gln Ala Asn Thr Leu Val
 465 470 475 480
 Asp Leu Ala Lys Thr Gln Asn Ile Met Tyr Asp Met Ile Ser Asp Leu
 485 490 495
 Asn Glu Arg Ser Glu Asp Phe Glu Lys Arg Ile Val Thr Leu Glu Thr
 500 505 510
 Lys Leu Glu Thr Leu Ile Gly Ser Ile His Ala Leu Pro Gly Leu Ile
 515 520 525
 Ser Gln Thr Ile Arg Gln Gln Gln Arg Asp Phe Ile Glu Ala Gln Met
 530 535 540
 Glu Ser Tyr Asp Lys His Val Thr Tyr Asn Ala Glu Arg Ser Arg Ser
 545 550 555 560
 Ser Ser Arg Arg Arg Arg Ser Ser Ser Thr Ala Pro Pro Thr Ser Ser
 565 570 575
 Glu Ser Ser

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 557 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..557
- (D) OTHER INFORMATION: /note= "N-terminally truncated form of human small conductance, calcium-activated potassium channel protein 3 (hSK3)"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 109..436
- (D) OTHER INFORMATION: /note= "core region of hSK3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Ser Ser Cys Lys Tyr Ser Gly Gly Val Met Lys Pro Leu Ser Arg
 1 5 10 15
 Leu Ser Ala Ser Arg Arg Asn Leu Ile Glu Ala Glu Thr Glu Gly Gln
 20 25 30

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Pro Leu Gln Leu Phe Ser Pro Ser Asn Pro Pro Glu Ile Val Ile Ser
 35 40 45
 Ser Arg Glu Asp Asn His Ala His Gln Thr Leu Leu His His Pro Asn
 50 55 60
 Ala Thr His Asn His Gln His Ala Gly Thr Thr Ala Ser Ser Thr Thr
 65 70 75 80
 Phe Pro Lys Ala Asn Lys Arg Lys Asn Gln Asn Ile Gly Tyr Lys Leu
 85 90 95
 Gly His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr
 100 105 110
 Ala Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Ile Glu Thr
 115 120 125
 Glu Leu Ser Trp Gly Leu Tyr Ser Lys Asp Ser Met Phe Ser Leu Ala
 130 135 140
 Leu Lys Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile
 145 150 155 160
 Ile Ala Tyr His Thr Arg Glu Val Gln Leu Phe Val Ile Asp Asn Gly
 165 170 175
 Ala Asp Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile Leu Tyr Ile
 180 185 190
 Ser Leu Glu Met Leu Val Cys Ala Ile His Pro Ile Pro Gly Glu Tyr
 195 200 205
 Lys Phe Phe Trp Thr Ala Arg Leu Ala Phe Ser Tyr Thr Pro Ser Arg
 210 215 220
 Ala Glu Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg
 225 230 235 240
 Leu Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr
 245 250 255
 Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn
 260 265 270
 Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val
 275 280 285
 Leu Leu Val Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val
 290 295 300
 Arg Val Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe
 305 310 315 320
 Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr
 325 330 335
 Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu
 340 345 350
 Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val
 355 360 365
 Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe
 370 375 380

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Met Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala Ala Ala Asn
 385 390 395 400

Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys
 405 410 415

Lys Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys Phe Leu Gln
 420 425 430

Ala Ile His Gln Leu Arg Ser Val Lys Met Glu Gln Arg Lys Leu Ser
 435 440 445

Asp Gln Ala Asn Thr Leu Val Asp Leu Ser Lys Met Gln Asn Val Met
 450 455 460

Tyr Asp Leu Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp Leu Glu Lys
 465 470 475 480

Gln Ile Gly Ser Leu Glu Ser Lys Leu Glu His Leu Thr Ala Ser Phe
 485 490 495

Asn Ser Leu Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln Gln Gln Gln
 500 505 510

Gln Leu Leu Ser Ala Ile Ile Glu Ala Arg Gly Val Ser Val Ala Val
 515 520 525

Gly Thr Thr His Thr Pro Ile Ser Asp Ser Pro Ile Gly Val Ser Ser
 530 535 540

Thr Ser Phe Pro Thr Pro Tyr Thr Ser Ser Ser Ser Cys
 545 550 555

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1740 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1740
 (D) OTHER INFORMATION: /note= "human small conductance,
 calcium-activated potassium channel protein 2 (hSK2) cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAGCAGCT GCAGGTACAA CGGGGGCGTC ATGCGGCCGC TCAGCAACTT GAGCGCGTCC 60

CGCCGGAACC TGCACGAGAT GGAATCAGAG GCGCAGCCCC TGCAGCCCCC CGCGTCTGTC 120

GGAGGAGGTG GCGGCGCGTC CTCCCCGTCT GCAGCCGCTG CCGCCGCCGC CGCTGTTTCG 180

TCCTCAGCCC CCGAGATCGT GGTGTCTAAG CCCGAGCACA ACAACTCCAA CAACCTGGCG 240

CTCTATGGAA CCGGCGGCGG AGGCAGCACT GGAGGAGGCG GCGGCGGTGG CGGGAGCGGG 300

CACGGCAGCA GCAGTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAAG 360

CTGGGCCACC GCGCGGCCCT GTTCGAAAAG CGCAAGCGGC TCAGCGACTA CGCGCTCATC 420

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TTCGGCATGT TCGGCATCGT GGTTCATGGTC ATCGAGACCG AGCTGTCGTG GGGCGCCTAC 480
GACAAGGCGT CGCTGTATTC CTTAGCTCTG AAATGCCTTA TCAGTCTCTC CACGATCATC 540
CTGCTCGGTC TGATCATCGT GTACCACGCC AGGGAATAC AGTTGTTTCAT GGTGGACAAT 600
GGAGCAGATG ACTGGAGAAT AGCCATGACT TATGAGCGTA TTTTCTTCAT CTGCTTGGAA 660
ATACTGGTGT GTGCTATTCA TCCCATACCT GGGGAATTATA CATTACATG GACGGCCCCG 720
CTTGCCCTTCT CCTATGCCCC ATCCACAACC ACCGCTGATG TGGATATTAT TTTATCTATA 780
CCAATGTTCT TAAGACTCTA TCTGATTGCC AGAGTCATGC TTTTACATAG CAAACTTTTC 840
ACTGATGCCT CCTCTAGAAG CATTGGAGCA CTTAATAAGA TAAACTTCAA TACACGTTTT 900
GTTATGAAGA CTTTAATGAC TATATGCCCC GGAAGTGTAC TCTTGGTTTT TAGTATCTCA 960
TTATGGATAA TTGCCGCATG GACTGTCCGA GCTTGTGAAA GGTACCATGA TCAACAGGAT 1020
GTTACTAGCA ACTTCCTTGG AGCGATGTGG TTGATATCAA TAACTTTTCT CTCCATTGGT 1080
TATGGTGACA TGGTACCTAA CACATACTGT GGAAAAGGAG TCTGCTTACT TACTGGAATT 1140
ATGGGTGCTG GTTGACACAGC CCTGGTGGTA GCTGTAGTGG CAAGGAAGCT AGAACTTACC 1200
AAAGCAGAAA AACACGTGCA CAATTTTCATG ATGGATACTC AGCTGACTAA AAGAGTAAAA 1260
AATGCAGCTG CCAATGTACT CAGGGAAACA TGGCTAATTT AAAAAATAC AAAGCTAGTG 1320
AAAAAGATAG ATCATGCAAA AGTAAGAAAA CATCAACGAA AATTCCTGCA AGCTATTTCAT 1380
CAATTAAGAA GTGTAAAAAT GGAACAGAGG AAAGTGAATG ACCAAGCAAA CACTTTGGTG 1440
GACTTGGCAA AGACCCAGAA CATCATGTAT GATATGATTT CTGACTTAAA CGAAAGGAGT 1500
GAAGACTTCG AGAAGAGGAT TGTTACCTTG GAAACAAAAT TAGAGACTTT GATTGGTAGC 1560
ATCCACGCCC TCCCTGGGCT CATAAGCCAG ACCATCAGGC AGCAGCAGAG AGATTTTCATT 1620
GAGGCTCAGA TGGAGAGCTA CGACAAGCAC GTCACCTACA ATGCTGAGCG GTCCCGGTCC 1680
TCGTCCAGGA GCGGCGGTC CTCTCCACA GCACCACCAA CTTTCATCAGA GAGTAGCTAG 1740

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1674 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1674
(D) OTHER INFORMATION: /note= "N-terminally truncated cDNA
for human small conductance, calcium-activated potassium channel
protein 3 (hSK3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAGCTCCT GCAAGTATAG CGGTGGGGTC ATGAAGCCCC TCAGCCGCCT CAGCGCCTCC	60
CGGAGGAACC TCATCGAGGC CGAGACTGAG GGCCAACCCC TCCAGCTTTT CAGCCCTAGC	120
AACCCCCCGG AGATCGTCAT CTCCTCCCGG GAGGACAACC ATGCCACCA GACCCTGCTC	180
CATCACCTTA ATGCCACCA CAACCACCAG CATGCCGGCA CCACCGCCAG CAGCACCACC	240
TTCCCCAAG CCAACAAGCG GAAAAACCA AACATTGGCT ATAAGCTGGG ACACAGGAGG	300
GCCCTGTTTG AAAAGAGAAA GCGACTGAGT GACTATGCTC TGATTTTTGG GATGTTTGGA	360
ATTGTTGTTA TGGTGATAGA GACCGAGCTC TCTTGGGGTT TGTACTCAA GGA CTCCATG	420
TTTTCGTTGG CCTTGAAATG CCTTATCAGT CTGTCCACCA TCATCCTTTT GGGCTTGATC	480
ATCGCCTACC ACACACGTGA AGTCCAGCTC TTCGTGATCG ACAACGGCGC GGATGACTGG	540
CGGATAGCCA TGACCTACGA GCGCATCCTC TACATCAGCC TGGAGATGCT GGTGTGCGCC	600
ATCCACCCCA TTCCTGGCGA GTACAAGTTC TTCTGGACGG CACGCCTGGC CTTCTCCTAC	660
ACACCCTCCC GGGCGGAGGC CGATGTGGAC ATCATCCTGT CTATCCCAT GTTCCTGCGC	720
CTGTACCTGA TCGCCCGAGT CATGCTGCTG CACAGCAAGC TCTTCACCGA TGCCTCGTCC	780
CGCAGCATCG GGGCCCTCAA CAAGATCAAC TTCAACACCC GCTTTGTCAT GAAGACGCTC	840
ATGACCATCT GCCCTGGCAC TGTGCTGCTC GTGTTAGCA TCTCTCTGTG GATCATTGCT	900
GCCTGGACCG TCCGTGTCTG TGAAAGGTAC CATGACCAGC AGGACGTAAC TAGTAAC TTT	960
CTGGGTGCCA TGTGGCTCAT CTCCATCACA TTCCTTTCCA TTGGTTATGG GGACATGGTG	1020
CCCCACACAT ACTGTGGGAA AGGTGTCTGT CTCCTCACTG GCATCATGGG TGCAGGCTGC	1080
ACTGCCCTTG TGGTGGCCGT GGTGGCCCGA AAGCTGGAAC TCACCAAAGC GGAGAAGCAC	1140
GTTCATAACT TCATGATGGA CACTCAGCTC ACCAAGCGGA TCAAGAATGC TGCAGCCAAT	1200
GTCCCTCGGG AAACATGGTT AATCTATAAA CACACAAAGC TGCTAAAGAA GATTGACCAT	1260
GCCAAAGTGA GGAAACACCA GAGGAAGTTC CTCCAAGCTA TCCACCAGTT GAGGAGCGTC	1320
AAGATGGAAC AGAGGAAGCT GAGTGACCAA GCCAACACTC TGGTGGACCT TTCCAAGATG	1380
CAGAATGTCA TGTATGACTT AATCACAGAA CTCAATGACC GGAGCGAAGA CCTGGAGAAG	1440
CAGATTGGCA GCCTGGAGTC GAAGCTGGAG CATCTACCG CCAGCTTCAA CTCCCTGCCG	1500
CTGCTCATCG CCGACACCTT GCGCCAGCAG CAGCAGCAGC TCCTGTCTGC CATCATCGAG	1560
GCCCCGGGTG TCAGCGTGGC AGTGGGCACC ACCCACCCC CAATCTCCGA TAGCCCCATT	1620
GGGGTCAGCT CCACCTCCTT CCGACCCCG TACACAAGTT CAAGCAGTTG CTAA	1674

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGAGCAGCT GCAGGTACAA CG

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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAGCTACTC TCTGATGAAG TTG

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGAGCTCCT GCAAGTATAG C

21

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTAGCAACTG CTTGAACTTG TG

22

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

114

(ix) FEATURE:

- (A) NAME/KEY: Region
 (B) LOCATION: 1..328
 (D) OTHER INFORMATION: /note= "core region of hSK1 from amino acid positions 124 through 451"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Ser Asp Tyr Ala Leu Ile Phe Gly Met Phe Gly Ile Val Val Met
 1 5 10 15
 Val Thr Glu Thr Glu Leu Ser Trp Gly Val Tyr Thr Lys Glu Ser Leu
 20 25 30
 Tyr Ser Phe Ala Leu Lys Cys Leu Ile Ser Leu Ser Thr Ala Ile Leu
 35 40 45
 Leu Gly Leu Val Val Leu Tyr His Ala Arg Glu Ile Gln Leu Phe Met
 50 55 60
 Val Asp Asn Gly Ala Asp Asp Trp Arg Ile Ala Met Thr Cys Glu Arg
 65 70 75 80
 Val Phe Leu Ile Ser Leu Glu Leu Ala Val Cys Ala Ile His Pro Val
 85 90 95
 Pro Gly His Tyr Arg Phe Thr Trp Thr Ala Arg Leu Ala Phe Thr Tyr
 100 105 110
 Ala Pro Ser Val Ala Glu Ala Asp Val Asp Val Leu Leu Ser Ile Pro
 115 120 125
 Met Phe Leu Arg Leu Tyr Leu Leu Gly Arg Val Met Leu Leu His Ser
 130 135 140
 Lys Ile Phe Thr Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys
 145 150 155 160
 Ile Thr Phe Asn Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys
 165 170 175
 Pro Gly Thr Val Leu Leu Val Phe Ser Ile Ser Ser Trp Ile Ile Ala
 180 185 190
 Ala Trp Thr Val Arg Val Cys Glu Arg Tyr His Asp Lys Gln Glu Val
 195 200 205
 Thr Ser Asn Phe Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu
 210 215 220
 Ser Ile Gly Tyr Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly
 225 230 235 240
 Val Cys Leu Leu Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val
 245 250 255
 Val Ala Val Val Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His
 260 265 270
 Val His Asn Phe Met Met Asp Thr Gln Leu Thr Lys Arg Val Lys Asn
 275 280 285
 Ala Ala Ala Asn Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr
 290 295 300

115

Arg Leu Val Lys Lys Pro Asp Gln Ala Arg Val Arg Lys His Gln Arg
 305 310 315 320

Lys Phe Leu Gln Ala Ile His Gln
 325

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gly His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Phe Thr Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe
 1 5 10 15

Met Met Asp Thr Gln Leu Thr Lys Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1287
(D) OTHER INFORMATION: /note= "human intermediate
conductance, calcium-activated potassium channel protein 1
(hIK1) cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGGCGGGG ATCTGGTGCT TGGCCTGGGG GCCTTGAGAC GCCGAAAGCG CTTGCTGGAG 60
CAGGAGAAGT CTCTGGCCGG CTGGGCACTG GTGCTGGCAG GAACTGGCAT TGGACTCATG 120
GTGCTGCATG CAGAGATGCT GTGGTTCGGG GGGTGCTCGT GGGCGCTCTA CCTGTTCCTG 180
GTTAAATGCA CGATCAGCAT TTCCACCTTC TTA CTCTCTT GCCTCATCGT GGCCTTTTCAT 240
GCCAAAGAGG TCCAGCTGTT CAGTACCGAC AACGGGCTGC GGGACTGGCG CGTGGTGCTC 300
CTGACCGGGC GGCAGGCGGC GCAGATCGTG CTGGAGCTGG TGGTGTGTGG GCTGCACCCG 360
GCGCCCGTGC GGGGCCCCGCC GTGCGTGCG GATTTAGGGG CGCCGCTGAC CTCCCCGCAG 420
CCCTGGCCGG GATTCCTGGG CCAAGGGGAA GCGCTGCTGT CCCTGGCCAT GCTGCTGCGT 480
CTCTACCTGG TGCCCCGCGC CGTGCTCCTG CGCAGCGGCG TCCTGCTCAA CGCTTCCTAC 540
CGCAGCATCG GCGCTCTCAA TCAAGTCCGC TTCCGCCACT GGTTCGTGGC CAAGCTTTAC 600
ATGAACACGC ACCCTGGCCG CCTGTGCTC GGCCTCACGC TTGGCCTCTG GCTGACCACC 660
GCCTGGGTGC TGTCCGTGGC CGAGAGGCAG GCTGTTAATG CCACTGGGCA CCTTTCAGAC 720
ACACTTTGGC TGATCCCCAT CACATTCCTG ACCATCGGCT ATGGTGACGT GGTGCCGGGC 780
ACCATGTTGG GCAAGATCGT CTGCCTGTGC ACTGGAGTCA TGGGTGTCTG CTGCACAGCC 840
CTGCTGGTGG CCGTGGTGGC CCGGAAGCTG GAGTTTAAAC AGGCAGAGAA GCACGTGCAC 900
AACTTCATGA TGGATATCCA GAATACCAA GAGATGAAG AGTCCGCTGC CCGAGTGCTA 960
CAAGAAGCCT GGATGTTCTA CAAACATACT CGCAGGAAG AGTCTCATGC TGCCCGCAGG 1020
CATCAGCGCA AGCTGCTGGC CGCCATCAAC GCGTTCCGCC AGGTGCGGCT GAAACACCGG 1080
AAGCTCCGGG AACAAGTGAA CTCCATGGTG GACATCTCCA AGATGCACAT GATCCTGTAT 1140
GACCTGCAGC AGAATCTGAG CAGCTCACAC CGGGCCCTGG AGAAACAGAT TGACACGCTG 1200
GCGGGGAAGC TGGATGCCCT GACTGAGCTG CTTAGCACTG CCCTGGGGCC GAGGCAGCTT 1260
CCAGAACCCA GCCAGCAGTC CAAGTAG 1287

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..428
- (D) OTHER INFORMATION: /note= "human intermediate conductance, calcium-activated potassium channel protein 1 (hIK1)"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 25..351
- (D) OTHER INFORMATION: /note= "core region of hIK1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

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Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg Lys
1           5           10           15
Arg Leu Leu Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu
20          25          30
Ala Gly Thr Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp
35          40          45
Phe Gly Gly Cys Ser Trp Ala Leu Tyr Leu Phe Leu Val Lys Cys Thr
50          55          60
Ile Ser Ile Ser Thr Phe Leu Leu Leu Cys Leu Ile Val Ala Phe His
65          70          75          80
Ala Lys Glu Val Gln Leu Phe Ser Thr Asp Asn Gly Leu Arg Asp Trp
85          90          95
Arg Val Val Leu Leu Thr Gly Arg Gln Ala Ala Gln Ile Val Leu Glu
100         105         110
Leu Val Val Cys Gly Leu His Pro Ala Pro Val Arg Gly Pro Pro Cys
115         120         125
Val Gln Asp Leu Gly Ala Pro Leu Thr Ser Pro Gln Pro Trp Pro Gly
130         135         140
Phe Leu Gly Gln Gly Glu Ala Leu Leu Ser Leu Ala Met Leu Leu Arg
145         150         155         160
Leu Tyr Leu Val Pro Arg Ala Val Leu Leu Arg Ser Gly Val Leu Leu
165         170         175
Asn Ala Ser Tyr Arg Ser Ile Gly Ala Leu Asn Gln Val Arg Phe Arg
180         185         190
His Trp Phe Val Ala Lys Leu Tyr Met Asn Thr His Pro Gly Arg Leu
195         200         205
Leu Leu Gly Leu Thr Leu Gly Leu Trp Leu Thr Thr Ala Trp Val Leu
210         215         220

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Ser Val Ala Glu Arg Gln Ala Val Asn Ala Thr Gly His Leu Ser Asp
 225 230 235 240
 Thr Leu Trp Leu Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr Gly Asp
 245 250 255
 Val Val Pro Gly Thr Met Leu Gly Lys Ile Val Cys Leu Cys Thr Gly
 260 265 270
 Val Met Gly Val Cys Cys Thr Ala Leu Leu Val Ala Val Val Ala Arg
 275 280 285
 Lys Leu Glu Phe Asn Lys Ala Glu Lys His Val His Asn Phe Met Met
 290 295 300
 Asp Ile Gln Asn Thr Lys Glu Met Lys Glu Ser Ala Ala Arg Val Leu
 305 310 315 320
 Gln Glu Ala Trp Met Phe Tyr Lys His Thr Arg Arg Lys Glu Ser His
 325 330 335
 Ala Ala Arg Arg His Gln Arg Lys Leu Leu Ala Ala Ile Asn Ala Phe
 340 345 350
 Arg Gln Val Arg Leu Lys His Arg Lys Leu Arg Glu Gln Val Asn Ser
 355 360 365
 Met Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln
 370 375 380
 Asn Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu
 385 390 395 400
 Ala Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly
 405 410 415
 Pro Arg Gln Leu Pro Glu Pro Ser Gln Gln Ser Lys
 420 425

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Arg Gly Pro Pro Cys Val Gln Asp Leu Gly Ala Pro Leu Thr Ser
 1 5 10 15
 Pro Gln Pro Trp Pro Gly Phe Leu Gly Gln Gly Glu Ala Leu
 20 25 30

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

119

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCGTGCGTG CAGGATTTAG G

21

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCAGAGGCCA AGCGTGAGGC C

21

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TCCAAGATGC ACATGATCCT G

21

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGACTGCTGG CTGGGTTCTG G

21

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGGGCGGGG ATCTGGTGCT TG

22

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTACTTGAC TGCTGGCTGG GTTC

24

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGGCGGGG ATCTGGTGCT TGG

23

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGGTCCAGCT ACTTGACTG CTG

23

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ala	Arg	Lys	Leu	Glu	Leu	Thr	Lys	Ala	Glu	Lys	His	Val	His	Asn	Phe
1				5					10					15	
Met	Met	Asp	Thr	Gln	Leu	Thr	Lys								
				20											

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 732 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..732
- (D) OTHER INFORMATION: /note= "full-length rat small conductance, calcium-activated potassium channel protein 3 (rSK3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Asp	Thr	Ser	Gly	His	Phe	His	Glu	Ser	Gly	Val	Gly	Asp	Leu	Asp
1				5				10						15	
Glu	Asp	Pro	Lys	Cys	Pro	Cys	Pro	Ser	Ser	Gly	Asp	Glu	Gln	Gln	Gln
		20						25					30		
Gln	Gln	Gln	Pro	Pro	Pro	Pro	Ser	Ala	Pro	Pro	Ala	Val	Pro	Gln	Gln
		35					40				45				
Pro	Pro	Gly	Pro	Leu	Leu	Gln	Pro	Gln	Pro	Pro	Gln	Leu	Gln	Gln	Gln
		50				55					60				
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln
65				70				75						80	
Ala	Pro	Leu	His	Pro	Leu	Pro	Gln	Leu	Ala	Gln	Leu	Gln	Ser	Gln	Val
			85					90						95	
Val	His	Pro	Gly	Leu	Leu	His	Ser	Ser	Pro	Thr	Ala	Phe	Arg	Ala	Pro
			100					105					110		
Asn	Ser	Ala	Asn	Ser	Thr	Ala	Ile	Leu	His	Pro	Ser	Ser	Arg	Gln	Gly
		115					120					125			
Ser	Gln	Leu	Asn	Leu	Asn	Asp	His	Leu	Val	Gly	His	Ser	Pro	Ser	Ser
		130				135					140				
Thr	Ala	Thr	Ser	Gly	Pro	Gly	Gly	Gly	Ser	Arg	His	Arg	Gln	Ala	Ser
145					150				155					160	
Pro	Val	Val	His	Arg	Arg	Asp	Ser	Asn	Pro	Phe	Thr	Glu	Ile	Ala	Met
				165					170					175	
Ser	Ser	Cys	Lys	Tyr	Ser	Gly	Gly	Val	Met	Lys	Pro	Leu	Ser	Arg	Leu
			180					185					190		

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Ser Ala Ser Arg Arg Asn Leu Ile Glu Ala Glu Pro Glu Gly Gln Pro
 195 200 205
 Leu Gln Leu Phe Ser Pro Ser Asn Pro Pro Glu Ile Ile Ile Ser Ser
 210 215 220
 Arg Glu Asp Asn His Ala His Gln Thr Leu Leu His His Pro Asn Ala
 225 230 235 240
 Thr His Asn His Gln His Ala Gly Thr Thr Ala Gly Ser Thr Thr Phe
 245 250 255
 Pro Lys Ala Asn Lys Arg Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly
 260 265 270
 His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala
 275 280 285
 Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Ile Glu Thr Glu
 290 295 300
 Leu Ser Trp Gly Leu Tyr Ser Lys Asp Ser Met Phe Ser Leu Ala Leu
 305 310 315 320
 Lys Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile
 325 330 335
 Ala Tyr His Thr Arg Glu Val Gln Leu Phe Val Ile Asp Asn Gly Ala
 340 345 350
 Asp Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile Leu Tyr Ile Ser
 355 360 365
 Leu Glu Met Leu Val Cys Ala Ile His Pro Ile Pro Gly Glu Tyr Lys
 370 375 380
 Phe Phe Trp Thr Ala Arg Leu Ala Phe Ser Tyr Thr Pro Ser Arg Ala
 385 390 395 400
 Glu Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg Leu
 405 410 415
 Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr Asp
 420 425 430
 Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr
 435 440 445
 Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu
 450 455 460
 Leu Met Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg
 465 470 475 480
 Val Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu
 485 490 495
 Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly
 500 505 510
 Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr
 515 520 525
 Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala
 530 535 540

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Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met
 545 550 555 560
 Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala Ala Ala Asn Val
 565 570 575
 Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys Lys
 580 585 590
 Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala
 595 600 605
 Ile His Gln Leu Arg Gly Val Lys Met Glu Gln Arg Lys Leu Ser Asp
 610 615 620
 Gln Ala Asn Thr Leu Val Asp Leu Ser Lys Met Gln Asn Val Met Tyr
 625 630 635 640
 Asp Leu Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp Leu Glu Lys Gln
 645 650 655
 Ile Gly Ser Leu Glu Ser Lys Leu Glu His Leu Thr Ala Ser Phe Asn
 660 665 670
 Ser Leu Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln Gln Gln Gln Gln
 675 680 685
 Leu Leu Thr Ala Phe Val Glu Ala Arg Gly Ile Ser Val Ala Val Gly
 690 695 700
 Thr Ser His Ala Pro Pro Ser Asp Ser Pro Ile Gly Ile Ser Ser Thr
 705 710 715 720
 Ser Phe Pro Thr Pro Tyr Thr Ser Ser Ser Ser Cys
 725 730

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2224
- (D) OTHER INFORMATION: /note= "rat small conductance, calcium-activated potassium channel protein 3 (rSK3) full-length cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CATGGACACT TCTGGGCACT TCCATGAGTC GGGGGTGGGG GATCTGGATG AAGACCCCAA 60
 GTGTCCCTGT CCATCTTCTG GGGACGAGCA ACAGCAGCAA CAGCAACCGC CACCACCGTC 120
 AGCGCCACCA GCAGTCCCCC AGCAGCCTCC GGGACCCTTG CTGCAGCCTC AGCCTCCGCA 180
 GCTTCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA 240
 GGCTCCACTG CACCCCCTGC CTCAGCTTGC CCAACTCCAG AGCCAGGTTG TCCATCCTGG 300

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TCTGTTGCAC TCTTCTCCCA CGGCTTTTCAG GGCTCCCAAT TCAGCCAACT CCACCGCCAT	360
CCTCCACCCT TCCTCCAGGC AAGGCAGCCA GCTAAATCTC AATGACCACT TGGTTGGCCA	420
CTCTCCAAGT TCCACAGCCA CAAGTGGGCC TGGTGGAGGC AGCCGGCACC GGCAGGCCAG	480
CCCCGTGGTG CACCGGCGGG ACAGCAATCC CTTACGGAG ATAGCTATGA GTCCTGCAA	540
ATACAGCGGT GGGGTCATGA AGCCCTCAG CCGCCTCAGC GCCTCTCGGA GAAACCTTAT	600
CGAGGCCGAG CCTGAGGGCC AACCCTCCA GCTCTTCAGT CCCAGCAACC CCCAGAGAT	660
TATCATCTCC TCCAGGGAGG ATAACCATGC CCACCAGACT CTGCTCCATC ACCCCAACGC	720
TACCCACAAC CACCAGCATG CCGGCACCAC TGCTGGCAGC ACCACCTTC CCAAAGCCAA	780
CAAGCGGAAA AACCAAAACA TTGGCTATAA GCTGGGCAC AGGAGGGCCC TGTGAAAA	840
GAGAAAGCGA CTGAGTGACT ATGCTCTGAT TTTTGGGATG TTTGGAATTG TTGTTATGGT	900
GATAGAGACC GAACTGTCTT GGGGTTTGTG CTCAAAGGAT TCCATGTTTT CGTTGGCCCT	960
GAAATGCCTT ATCAGTTTAT CCACCATCAT CCTGCTTGGT TTGATCATCG CCTACCACAC	1020
AAGGGAAGTA CAGCTCTTTG TGATCGACAA TGGTGCAGAT GACTGGCGGA TAGCCATGAC	1080
CTATGAGCGC ATCCTCTACA TCAGCCTGGA GATGCTGGTG TGCGCCATCC ACCCCATTCC	1140
TGGAGAGTAC AAGTTCTTCT GGACGGCAGC CCTGGCCTTC TCCTACACCC CCTCTCGGGC	1200
AGAGGCTGAC GTGGACATTA TTCTGTCCAT CCCCATGTTC TTGCGCCTAT ACCTGATCGC	1260
CCGAGTCATG CTGCTACATA GCAAGCTCTT CACGGATGCC TCATCCCGAA GCATCGGGGC	1320
CCTCAACAAG ATCAACTTCA ACACCCGATT CGTCATGAAG ACGCTCATGA CCATCTGCCC	1380
GGGCACGGTG CTGCTAATGT TCAGCATCTC TCTGTGGATC ATCGCTGCCT GGACTGTGAG	1440
AGTCTGTGAA AGGTACCATG ACCAGCAGGA CGTAACTAGT AACTTTCTGG GTGCCATGTG	1500
GCTCATCTCC ATCACGTTCC TTTCCATTGG CTATGGGGAC ATGGTGCCCC ACACATACTG	1560
TGGGAAAGGT GTCTGTCTTC TCACTGGCAT CATGGGTGCA GGCTGCACTG CCCTCGTGGT	1620
AGCTGTGGTT GCCCGGAAGC TCGAACTCAC CAAAGCAGAG AAGCATGTGC ACAACTTCAT	1680
GATGGACACT CAGCTCACCA AACGGATCAA GAACGCTGCC GCCAATGTCC TCCGGGAAAC	1740
ATGGCTGATC TACAAACACA CAAAGCTGCT AAAGAAGATT GACCACGCCA AAGTCAGGAA	1800
ACACCAGAGG AAGTTCCTCC AAGCTATTCA CCAACTGAGG GGTGTCAAGA TGAACAAAG	1860
GAAGCTGAGT GACCAAGCCA ACACCCTGGT GGACCTTTCC AAGATGCAGA ACGTCATGTA	1920
TGACTTGATC ACGGAGCTCA ACGACCGGAG TGAAGACCTG GAAAAGCAGA TTGGCAGCCT	1980
GGAATCCAAG CTGGAGCACC TCACAGCCAG CTTCAATTCC CTGCCCCTGC TCATCGCAGA	2040
CACCCTGCGC CAACAGCAGC AGCAGCTGCT CACTGCCTTC GTGGAGGCCC GGGGCATCAG	2100
TGTGGCTGTG GGAAGTAGCC ACGCCCCTCC CTCTGACAGC CCTATCGGGA TCAGCTCCAC	2160
CTCTTTCCCA ACCCCATACA CAAGTTCAAG CAGTTGCTAA ATAAACTCC CCACTCCAGA	2220
AGCA	2224

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(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Phe	Xaa	Ser	Ile	Pro	Xaa	Xaa	Xaa	Trp	Trp	Ala	Xaa	Val	Thr	Met	Thr
1				5				10						15	
Thr	Val	Gly	Tyr	Gly	Asp	Met	Xaa	Pro							
			20				25								

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Asn Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 736 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
(B) LOCATION: 1..736
(D) OTHER INFORMATION: /note= "full length human small
conductance, calcium-activated potassium channel protein 3
(hSK3)"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Asp Thr Ser Gly His Phe His Asp Ser Gly Val Gly Asp Leu Asp
 1 5 10 15
 Glu Asp Pro Lys Cys Pro Cys Pro Ser Ser Gly Asp Glu Gln Gln Gln
 20 25 30
 Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Ala Pro Pro
 35 40 45
 Ala Ala Pro Gln Gln Pro Leu Gly Pro Ser Leu Gln Pro Gln Pro Pro
 50 55 60
 Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 65 70 75 80
 Gln Gln Gln Gln Gln Pro Pro His Pro Leu Ser Gln Leu Ala Gln Leu
 85 90 95
 Gln Ser Gln Pro Val His Pro Gly Leu Leu His Ser Ser Pro Thr Ala
 100 105 110
 Phe Arg Ala Pro Pro Ser Ser Asn Ser Thr Ala Ile Leu His Pro Ser
 115 120 125
 Ser Arg Gln Gly Ser Gln Leu Asn Leu Asn Asp His Leu Leu Gly His
 130 135 140
 Ser Pro Ser Ser Thr Ala Thr Ser Gly Pro Gly Gly Gly Ser Arg His
 145 150 155 160
 Arg Gln Ala Ser Pro Leu Val His Arg Arg Asp Ser Asn Pro Ser Thr
 165 170 175
 Glu Ile Ala Met Ser Ser Cys Lys Tyr Ser Gly Gly Val Met Lys Pro
 180 185 190
 Leu Ser Arg Leu Ser Ala Ser Arg Arg Asn Leu Ile Glu Ala Glu Thr
 195 200 205
 Glu Gly Gln Pro Leu Gln Leu Phe Ser Pro Ser Asn Pro Pro Glu Ile
 210 215 220
 Val Ile Ser Ser Arg Glu Asp Asn His Ala His Gln Thr Leu Leu His
 225 230 235 240
 His Pro Asn Ala Thr His Asn His Gln His Ala Gly Thr Thr Ala Ser
 245 250 255
 Ser Thr Thr Phe Pro Lys Ala Asn Lys Arg Lys Asn Gln Asn Ile Gly
 260 265 270
 Tyr Lys Leu Gly His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu
 275 280 285
 Ser Asp Tyr Ala Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val
 290 295 300
 Ile Glu Thr Glu Leu Ser Trp Gly Leu Tyr Ser Lys Asp Ser Met Phe
 305 310 315 320
 Ser Leu Ala Leu Lys Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu
 325 330 335
 Gly Leu Ile Ile Ala Tyr His Thr Arg Glu Val Gln Leu Phe Val Ile
 340 345 350

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Asp Asn Gly Ala Asp Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile
 355 360 365
 Leu Tyr Ile Ser Leu Glu Met Leu Val Cys Ala Ile His Pro Ile Pro
 370 375 380
 Gly Glu Tyr Lys Phe Phe Trp Thr Ala Arg Leu Ala Phe Ser Tyr Thr
 385 390 395 400
 Pro Ser Arg Ala Glu Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met
 405 410 415
 Phe Leu Arg Leu Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser Lys
 420 425 430
 Leu Phe Thr Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile
 435 440 445
 Asn Phe Asn Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro
 450 455 460
 Gly Thr Val Leu Leu Val Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala
 465 470 475 480
 Trp Thr Val Arg Val Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr
 485 490 495
 Ser Asn Phe Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser
 500 505 510
 Ile Gly Tyr Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val
 515 520 525
 Cys Leu Leu Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val
 530 535 540
 Ala Val Val Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val
 545 550 555 560
 His Asn Phe Met Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala
 565 570 575
 Ala Ala Asn Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys
 580 585 590
 Leu Leu Lys Lys Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys
 595 600 605
 Phe Leu Gln Ala Ile His Gln Leu Arg Ser Val Lys Met Glu Gln Arg
 610 615 620
 Lys Leu Ser Asp Gln Ala Asn Thr Leu Val Asp Leu Ser Lys Met Gln
 625 630 635 640
 Asn Val Met Tyr Asp Leu Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp
 645 650 655
 Leu Glu Lys Gln Ile Gly Ser Leu Glu Ser Lys Leu Glu His Leu Thr
 660 665 670
 Ala Ser Phe Asn Ser Leu Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln
 675 680 685
 Gln Gln Gln Gln Leu Leu Ser Ala Ile Ile Glu Ala Arg Gly Val Ser
 690 695 700

128

Val Ala Val Gly Thr Thr His Thr Pro Ile Ser Asp Ser Pro Ile Gly
 705 710 715 720
 Val Ser Ser Thr Ser Phe Pro Thr Pro Tyr Thr Ser Ser Ser Ser Cys
 725 730 735

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..2462
 (D) OTHER INFORMATION: /note= "human small conductance,
 calcium-activated potassium channel protein 3 (hSK3) full length
 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AGTTCTTTCA CCCCTCTTC TTTCTCCAAG CTCCCCTCCT GCTCTCCCTC CCTGCCCAAT 60
 ACAATGCATT CTTGAGTGGC AGCGTCTGGA CTCCAGGCAG CCCAGAGAA CCGAAGCAAG 120
 CCAAAGAGAG GACTGGAGCC AAGATACTGG TGGGGGAGAT TGGATGCCTG GCTTTCTTTG 180
 AGGACATCTT TGGAGCGAGG GTGGCTTTGG GGTGGGGGCT TGTGCTGCAG GGAATACAGC 240
 CAGGCCCCAA GATGGACACT TCTGGGCACT TCCATGACTC GGGGGTGGGG GACTTGGATG 300
 AAGACCCCAA GTGCCCCTGT CCATCCTCTG GGGATGAGCA GCAGCAGCAG CAGCAGCAGC 360
 AACAGCAGCA GCAGCCACCA CCGCCAGCGC CACCAGCAGC CCCCAGCAG CCCCTGGGAC 420
 CCTCGCTGCA GCCTCAGCCT CCGCAGCTTC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC 480
 AGCAGCAGCA GCAGCAGCAG CAGCAGCCAC CGCATCCCCT GTCTCAGCTC GCCCAACTCC 540
 AGAGCCAGCC CGTCCACCCT GGCCTGCTGC ACTCCTCTCC CACCGCTTTC AGGGCCCCCCC 600
 CTTCTGTCCTA CTCCACCGCC ATCCTCCACC CTTCCTCCAG GCAAGGCAGC CAGCTCAATC 660
 TCAATGACCA CTTGCTTGGC CACTCTCCAA GTTCCACAGC TACAAGTGGG CCTGGCGGAG 720
 GCAGCCGGCA CCGACAGGCC AGCCCCCTGG TGCACCGGCG GGACAGCAAC CCCTCCACGG 780
 AGATCGCCAT GAGCTCCTGC AAGTATAGCG GTGGGGTCAT GAAGCCCCCTC AGCCGCCTCA 840
 GCGCCTCCCG GAGGAACCTC ATCGAGGCCG AGACTGAGGG CCAACCCCTC CAGCTTTTCA 900
 GCCCTAGCAA CCCCCCGGAG ATCGTCATCT CCTCCCGGGA GGACAACCAT GCCCACCAGA 960
 CCCTGCTCCA TCACCTAAT GCCACCCACA ACCACCAGCA TGCCGGCACC ACCGCCAGCA 1020
 GCACCACCTT CCCCAGGCC AACAGCGGA AAAACCAAAA CATTGGCTAT AAGCTGGGAC 1080
 ACAGGAGGGC CCTGTTTGAA AAGAGAAAGC GACTGAGTGA CTATGCTCTG ATTTTGGGA 1140
 GTTTTGAAT TGTTGTTATG GTGATAGAGA CCGAGCTCTC TTGGGGTTTG TACTCAAAGG 1200

ACTCCATGTT TTCGTTGGCC CTGAAATGCC TTATCAGTCT GTCCACCATC ATCCTTTTGG 1260
GCTTGATCAT CGCCTAACCAC ACACGTGAAG TCCAGCTCTT CGTGATCGAC AACGGCGCGG 1320
ATGACTGGCG GATAGCCATG ACCTACGAGC GCATCCTCTA CATCAGCCTG GAGATGCTGG 1380
TGTGCGCCAT CCACCCCATT CCTGGCGAGT ACAAGTTCTT CTGGACGGCA CGCCTGGCCT 1440
TCTCCTACAC ACCCTCCCGG GCGGAGGCCG ATGTGGACAT CATCCTGTCT ATCCCATGT 1500
TCCTGCGCCT GTACCTGATC GCCCGAGTCA TGCTGTGCA CAGCAAGCTC TTCACCGATG 1560
CCTCGTCCCG CAGCATCGGG GCCCTCAACA AGATCAACTT CAACACCCGC TTTGTCTATGA 1620
AGACGCTCAT GACCATCTGC CCTGGCACTG TGCTGCTCGT GTTCAGCATC TCTCTGTGGA 1680
TCATTGCTGC CTGGACCGTC CGTGTCTGTG AAAGGTACCA TGACCAGCAG GACGTAACCTA 1740
GTAACCTTCT GGGTGCCATG TGGCTCATCT CCATCACATT CCTTTCCATT GGTATGGGG 1800
ACATGGTGCC CCACACATAC TGTGGGAAAG GTGTCTGTCT CCTCACTGGC ATCATGGGTG 1860
CAGGCTGCAC TGCCCTTG TGCGCCGTGG TGGCCCGAAA GCTGGAATC ACCAAAGCGG 1920
AGAAGCACGT TCATAACTTC ATGATGGACA CTCAGCTCAC CAAGCGGATC AAGAATGCTG 1980
CAGCCAATGT CCTTCGGGAA ACATGGTTAA TCTATAAACA CACAAAGCTG CTAAAGAAGA 2040
TTGACCATGC CAAAGTGAGG AAACACCAGA GGAAGTTCCT CCAAGCTATC CACCAGTTGA 2100
GGAGCGTCAA GATGGAACAG AGGAAGCTGA GTGACCAAGC CAACACTCTG GTGGACCTTT 2160
CCAAGATGCA GAATGTCATG TATGACTTAA TCACAGAACT CAATGACCGG AGCGAAGACC 2220
TGGAGAAGCA GATTGGCAGC CTGGAGTCTA AGCTGGAGCA TCTACCGCC AGCTTCAACT 2280
CCCTGCCGCT GCTCATCGCC GACACCCTGC GCCAGCAGCA GCAGCAGCTC CTGTCTGCCA 2340
TCATCGAGGC CCGGGGTGTC AGCGTGGCAG TGGGCACCAC CCACACCCCA ATCTCCGATA 2400
GCCCCATTGG GGTGAGCTCC ACCTCCTTCC CGACCCCGTA CACAAGTTCA AGCAGTTGCT 2460
AA